



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/517,905

DATE: 12/22/2004  
TIME: 16:05:53

Input Set : A:\335026.txt  
Output Set: N:\CRF4\12222004\J517905.raw

3 <110> APPLICANT: Oregon Health & Science University  
4 Michael, Heinrich Charles  
5 Corless, Christopher Lee  
6 Fletcher, Jonathan Alfred  
7 Demetri, George D.  
9 <120> TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR  
RECEPTOR

10 ALPHA (PDGFR) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS  
12 <130> FILE REFERENCE: 899-65892-02

C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/517,905

C--> 14 <141> CURRENT FILING DATE: 2004-12-10

14 <150> PRIOR APPLICATION NUMBER: US 60/389,107

15 <151> PRIOR FILING DATE: 2002-06-13

17 <150> PRIOR APPLICATION NUMBER: US 60/438,899

18 <151> PRIOR FILING DATE: 2003-01-08

20 <160> NUMBER OF SEQ ID NOS: 27

22 <170> SOFTWARE: PatentIn version 3.2

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 6633

26 <212> TYPE: DNA

27 <213> ORGANISM: Homo sapiens

30 <220> FEATURE:

31 <221> NAME/KEY: CDS

32 <222> LOCATION: (395)..(3664)

34 <400> SEQUENCE: 1

Does Not Comply  
Corrected Diskette Needed

P.6

35	ttctccccgc ccccccagttg ttgtcgaagt ctgggggttg ggactggacc ccctgattgc	60
37	gtaagagcaa aaagcgaaagg cgaatctgg acactggag attcggagcg cagggagttt	120
39	gagagaaaact tttattttga agagaccaag gttgaggggg ggcttatttc ctgacagcta	180
41	tttactttaga gcaaattgatt agttttagaa ggatggacta taacattgaa tcaattacaa	240
43	aacgcgggtt ttgagccat tactgttgg a gctacaggaa gagaaacagg aggagactgc	300
45	aagagatcat ttgggaaggc cgtgggcacg ctcttactc catgtgtgg acattcattg	360
47	cggaataaca tcggaggaga agtttcccag agt atg ggg act tcc cat ccg gcg	415
48	Met Gly Thr Ser His Pro Ala	
49	1 5	
51	ttc ctg gtc tta ggc tgt ctt ctc aca ggg ctg agc cta atc ctc tgc	463
52	Phe Leu Val Leu Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys	
53	10 15 20	
55	cag ctt tca tta ccc tct atc ctt cca aat gaa aat gaa aag gtt gtg	511
56	Gln Leu Ser Leu Pro Ser Ile Leu Pro Asn Glu Asn Lys Val Val	
57	25 30 35	
59	cag ctg aat tca tcc ttt tct ctg aga tgc ttt ggg gag agt gaa gtg	559
60	Gln Leu Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val	
61	40 45 50 55	
63	agc tgg cag tac ccc atg tct gaa gaa gag agc tcc gat gtg gaa atc	607

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64	Ser	Trp	Gln	Tyr	Pro	Met	Ser	Glu	Glu	Glu	Ser	Ser	Asp	Val	Glu	Ile	
65					60			65						70			
67	aga	aat	gaa	gaa	aac	aac	agc	ggc	ctt	ttt	gtg	acg	gtc	ttg	gaa	gtg	655
68	Arg	Asn	Glu	Glu	Asn	Asn	Ser	Gly	Leu	Phe	Val	Thr	Val	Leu	Glu	Val	
69					75				80					85			
71	agc	agt	gcc	tcg	gcg	gcc	cac	aca	ggg	ttt	tac	act	tgc	tat	tac	aac	703
72	Ser	Ser	Ala	Ala	Ala	His	Thr	Gly	Leu	Tyr	Thr	Cys	Tyr	Tyr	Asn		
73					90				95			100					
75	cac	act	cag	aca	gaa	gag	aat	gag	ctt	gaa	ggc	agg	cac	att	tac	atc	751
76	His	Thr	Gln	Thr	Glu	Glu	Asn	Glu	Leu	Glu	Gly	Arg	His	Ile	Tyr	Ile	
77					105			110				115					
79	tat	gtg	cca	gac	cca	gat	gta	gcc	ttt	gta	cct	cta	gga	atg	acg	gat	799
80	Tyr	Val	Pro	Asp	Pro	Asp	Val	Ala	Phe	Val	Pro	Leu	Gly	Met	Thr	Asp	
81	120				125				130				135				
83	tat	tta	gtc	atc	gtg	gag	gat	gat	gat	tct	gcc	att	ata	cct	tgt	cgc	847
84	Tyr	Leu	Val	Ile	Val	Glu	Asp	Asp	Asp	Ser	Ala	Ile	Ile	Pro	Cys	Arg	
85					140				145			150					
87	aca	act	gat	ccc	gag	act	cct	gta	acc	tta	cac	aac	agt	gag	ggg	gtg	895
88	Thr	Thr	Asp	Pro	Glu	Thr	Pro	Val	Thr	Leu	His	Asn	Ser	Glu	Gly	Val	
89					155				160			165					
91	gta	cct	gcc	tcc	tac	gac	agc	aga	cag	ggc	ttt	aat	ggg	acc	ttc	act	943
92	Val	Pro	Ala	Ser	Tyr	Asp	Ser	Arg	Gln	Gly	Phe	Asn	Gly	Thr	Phe	Thr	
93					170			175			180						
95	gta	ggg	ccc	tat	atc	tgt	gag	gcc	acc	gtc	aaa	gga	aag	aag	ttc	cag	991
96	Val	Gly	Pro	Tyr	Ile	Cys	Glu	Ala	Thr	Val	Lys	Gly	Lys	Lys	Phe	Gln	
97					185			190			195						
99	acc	atc	cca	ttt	aat	gtt	tat	gct	tta	aaa	gca	aca	tca	gag	ctg	gat	1039
100	Thr	Ile	Pro	Phe	Asn	Val	Tyr	Ala	Leu	Lys	Ala	Thr	Ser	Glu	Leu	Asp	
101	200				205				210			215					
103	cta	gaa	atg	gaa	gct	ctt	aaa	acc	gtg	tat	aag	tca	ggg	gaa	acg	att	1087
104	Leu	Glu	Met	Glu	Ala	Leu	Lys	Thr	Val	Tyr	Lys	Ser	Gly	Glu	Thr	Ile	
105					220				225			230					
107	gtg	gtc	acc	tgt	gct	ttt	aac	aat	gag	gtg	ttt	gac	ctt	caa	tgg		1135
108	Val	Val	Thr	Cys	Ala	Val	Phe	Asn	Asn	Glu	Val	Val	Asp	Leu	Gln	Trp	
109					235			240			245						
111	act	tac	cct	gga	gaa	gtg	aaa	ggc	aaa	ggc	atc	aca	atg	ctg	gaa	gaa	1183
112	Thr	Tyr	Pro	Gly	Glu	Val	Lys	Gly	Lys	Gly	Ile	Thr	Met	Leu	Glu	Glu	
113					250			255			260						
115	atc	aaa	gtc	cca	tcc	atc	aaa	ttg	gtg	tac	act	ttg	acg	gtc	ccc	gag	1231
116	Ile	Lys	Val	Pro	Ser	Ile	Lys	Leu	Val	Tyr	Thr	Leu	Thr	Val	Pro	Glu	
117					265			270			275						
119	gcc	acg	gtg	aaa	gac	agt	gga	gat	tac	gaa	tgt	gct	gcc	cgc	cag	gct	1279
120	Ala	Thr	Val	Lys	Asp	Ser	Gly	Asp	Tyr	Glu	Cys	Ala	Ala	Arg	Gln	Ala	
121	280				285				290			295					
123	acc	agg	gag	gtc	aaa	gaa	atg	aag	aaa	gtc	act	att	tct	gtc	cat	gag	1327
124	Thr	Arg	Glu	Val	Lys	Glu	Met	Lys	Lys	Val	Thr	Ile	Ser	Val	His	Glu	
125					300			305			310						
127	aaa	ggt	ttc	att	gaa	atc	aaa	ccc	acc	ttc	agc	cag	ttg	gaa	gct	gtc	1375
128	Lys	Gly	Phe	Ile	Glu	Ile	Lys	Pro	Thr	Phe	Ser	Gln	Leu	Glu	Ala	Val	

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129	315	320	325													
131 aac	ctg	cat	gaa	gtc	aaa	cat	ttt	gtt	qta	gag	qtg	cgq	gcc	tac	cca	1423
132 Asn	Leu	His	Glu	Val	Lys	His	Phe	Val	Val	Glu	Val	Arg	Ala	Tyr	Pro	
133	330		335			340										
135 cct	ccc	agg	ata	tcc	tgg	ctg	aaa	aac	aat	ctg	act	ctg	att	gaa	aat	1471
136 Pro	Pro	Arg	Ile	Ser	Trp	Leu	Lys	Asn	Asn	Leu	Thr	Leu	Ile	Glu	Asn	
137	345		350			355										
139 ctc	act	gag	atc	acc	act	gat	gtg	gaa	aag	att	cag	gaa	ata	agg	tat	1519
140 Leu	Thr	Glu	Ile	Thr	Thr	Asp	Val	Glu	Lys	Ile	Gln	Glu	Ile	Arg	Tyr	
141	360		365			370									375	
143 cga	agc	aaa	tta	aag	ctg	atc	cgt	gct	aag	gaa	gaa	gac	agt	ggc	cat	1567
144 Arg	Ser	Lys	Leu	Lys	Leu	Ile	Arg	Ala	Lys	Glu	Glu	Asp	Ser	Gly	His	
145			380			385									390	
147 tat	act	att	gta	gct	caa	aat	gaa	gat	gct	gtg	aag	agc	tat	act	ttt	1615
148 Tyr	Thr	Ile	Val	Ala	Gln	Asn	Glu	Asp	Ala	Val	Lys	Ser	Tyr	Thr	Phe	
149			395			400									405	
151 gaa	ctg	tta	act	caa	gtt	cct	tca	tcc	att	ctg	gac	ttg	gtc	gat	gat	1663
152 Glu	Leu	Leu	Thr	Gln	Val	Pro	Ser	Ser	Ile	Leu	Asp	Leu	Val	Asp	Asp	
153			410			415									420	
155 cac	cat	ggc	tca	act	ggg	gga	cag	acg	gtg	agg	tgc	aca	gct	gaa	ggc	1711
156 His	His	Gly	Ser	Thr	Gly	Gly	Gln	Thr	Val	Arg	Cys	Thr	Ala	Glu	Gly	
157			425			430									435	
159 acg	ccg	ctt	cct	gat	att	gag	tgg	atg	ata	tgc	aaa	gat	att	aag	aaa	1759
160 Thr	Pro	Leu	Pro	Asp	Ile	Glu	Trp	Met	Ile	Cys	Lys	Asp	Ile	Lys	Lys	
161	440				445					450					455	
163 tgt	aat	aat	gaa	act	tcc	tgg	act	att	ttg	gcc	aac	aat	gtc	tca	aac	1807
164 Cys	Asn	Asn	Glu	Thr	Ser	Trp	Thr	Ile	Leu	Ala	Asn	Asn	Val	Ser	Asn	
165					460					465					470	
167 atc	atc	acg	gag	atc	cac	tcc	cga	gac	agg	agt	acc	gtg	gag	ggc	cgt	1855
168 Ile	Ile	Thr	Glu	Ile	His	Ser	Arg	Asp	Arg	Ser	Thr	Val	Glu	Gly	Arg	
169					475					480					485	
171 gtg	act	tcc	gcc	aaa	gtg	gag	gag	acc	atc	gcc	gtg	cga	tgc	ctg	gtc	1903
172 Val	Thr	Phe	Ala	Lys	Val	Glu	Glu	Thr	Ile	Ala	Val	Arg	Cys	Leu	Ala	
173			490			495									500	
175 aag	aat	ctc	ctt	gga	gct	gag	aac	cga	gag	ctg	aag	ctg	gtg	gct	ccc	1951
176 Lys	Asn	Leu	Leu	Gly	Ala	Glu	Asn	Arg	Glu	Leu	Lys	Leu	Val	Ala	Pro	
177			505			510									515	
179 acc	ctg	cgt	tct	gaa	ctc	acg	gtg	gct	gca	gtc	ctg	gtg	ctg	ttg		1999
180 Thr	Leu	Arg	Ser	Glu	Leu	Thr	Val	Ala	Ala	Ala	Val	Leu	Val	Leu	Leu	
181	520				525					530					535	
183 gtg	att	gtg	atc	atc	tca	ctt	att	gtc	ctg	gtt	gtc	att	tgg	aaa	cag	2047
184 Val	Ile	Val	Ile	Ile	Ser	Leu	Ile	Val	Leu	Val	Val	Ile	Trp	Lys	Gln	
185					540					545					550	
187 aaa	ccg	agg	tat	gaa	att	cgc	tgg	agg	gtc	att	gaa	tca	atc	agc	ccg	2095
188 Lys	Pro	Arg	Tyr	Glu	Ile	Arg	Trp	Arg	Val	Ile	Glu	Ser	Ile	Ser	Pro	
189					555					560					565	
191 gat	gga	cat	gaa	tat	att	tat	gtg	gac	ccg	atg	cag	ctg	cct	tat	gac	2143
192 Asp	Gly	His	Glu	Tyr	Ile	Tyr	Val	Asp	Pro	Met	Gln	Leu	Pro	Tyr	Asp	
193			570			575									580	

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195 tca aga tgg gag ttt cca aga gat gga cta gtg ctt ggt cgg gtc ttg	2191
196 Ser Arg Trp Glu Phe Pro Arg Asp Gly Leu Val Leu Gly Arg Val Leu	
197 585 590 595	
199 ggg tct gga gcg ttt ggg aag gtg gtt gaa gga aca gcc tat gga tta	2239
200 Gly Ser Gly Ala Phe Gly Lys Val Val Glu Gly Thr Ala Tyr Gly Leu	
201 600 605 610 615	
203 agc cgg tcc caa cct gtc atg aaa gtt gca gtg aag atg cta aaa ccc	2287
204 Ser Arg Ser Gln Pro Val Met Lys Val Ala Val Lys Met Leu Lys Pro	
205 620 625 630	
207 acg gcc aga tcc agt gaa aaa caa gct ctc atg tct gaa ctg aag ata	2335
208 Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile	
209 635 640 645	
211 atg act cac ctg ggg cca cat ttg aac att gta aac ttg ctg gga gcc	2383
212 Met Thr His Leu Gly Pro His Leu Asn Ile Val Asn Leu Leu Gly Ala	
213 650 655 660	
215 tgc acc aag tca ggc ccc att tac atc atc aca gag tat tgc ttc tat	2431
216 Cys Thr Lys Ser Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr	
217 665 670 675	
219 gga gat ttg gtc aac tat ttg cat aag aat agg gat agc ttc ctg agc	2479
220 Gly Asp Leu Val Asn Tyr Leu His Lys Asn Arg Asp Ser Phe Leu Ser	
221 680 685 690 695	
223 cac cac cca gag aag cca aag aaa gag ctg gat atc ttt gga ttg aac	2527
224 His His Pro Glu Lys Pro Lys Lys Glu Leu Asp Ile Phe Gly Leu Asn	
225 700 705 710	
227 cct gct gat gaa agc aca cgg agc tat gtt att tta tct ttt gaa aac	2575
228 Pro Ala Asp Glu Ser Thr Arg Ser Tyr Val Ile Leu Ser Phe Glu Asn	
229 715 720 725	
231 aat ggt gac tac atg gac atg aag cag gct gat act aca cag tat gtc	2623
232 Asn Gly Asp Tyr Met Asp Met Lys Gln Ala Asp Thr Thr Gln Tyr Val	
233 730 735 740	
235 ccc atg cta gaa agg aaa gag gtt tct aaa tat tcc gac atc cag aga	2671
236 Pro Met Leu Glu Arg Lys Glu Val Ser Lys Tyr Ser Asp Ile Gln Arg	
237 745 750 755	
239 tca ctc tat gat cgt cca gcc tca tat aag aag aaa tct atg tta gac	2719
240 Ser Leu Tyr Asp Arg Pro Ala Ser Tyr Lys Lys Ser Met Leu Asp	
241 760 765 770 775	
243 tca gaa gtc aaa aac ctc ctt tca gat gat aac tca gaa ggc ctt act	2767
244 Ser Glu Val Lys Asn Leu Leu Ser Asp Asp Asn Ser Glu Gly Leu Thr	
245 780 785 790	
247 tta ttg gat ttg ttg agc ttc acc tat caa gtt gcc cga gga atg gag	2815
248 Leu Leu Asp Leu Leu Ser Phe Thr Tyr Gln Val Ala Arg Gly Met Glu	
249 795 800 805	
251 ttt ttg gct tca aaa aat tgt gtc cac cgt gat ctg gct gct cgc aac	2863
252 Phe Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn	
253 810 815 820	
255 gtc ctc ctg gca caa gga aaa att gtg aag atc tgt gac ttt ggc ctg	2911
256 Val Leu Leu Ala Gln Gly Lys Ile Val Lys Ile Cys Asp Phe Gly Leu	
257 825 830 835	
259 gcc aga gac atc atg cat gat tcg aac tat gtg tcg aaa ggc agt acc	2959

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263	ttt	ctg	ccc	gtg	aag	tgg	atg	gct	gag	agc	atc	ttt	gac	aac	ctc		3007
264	Phe	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asp	Asn	Leu	
265					860					865						870	
267	tac	acc	aca	ctg	agt	gat	gtc	tgg	tct	tat	ggc	att	ctg	ctc	tgg	gag	
268	Tyr	Thr	Leu	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu		
269					875					880						885	
271	atc	ttt	tcc	ctt	ggc	acc	cct	tac	ccc	ggc	atg	atg	gtg	gat	tct		3103
272	Ile	Phe	Ser	Leu	Gly	Gly	Thr	Pro	Tyr	Pro	Gly	Met	Met	Val	Asp	Ser	
273					890					895						900	
275	act	ttc	tac	aat	aag	atc	aag	agt	ggg	tac	cgg	atg	gcc	aag	cct	gac	
276	Thr	Phe	Tyr	Asn	Lys	Ile	Lys	Ser	Gly	Tyr	Arg	Met	Ala	Lys	Pro	Asp	
277					905					910						915	
279	cac	gct	acc	agt	gaa	gtc	tac	gag	atc	atg	gtg	aaa	tgc	tgg	aac	agt	
280	His	Ala	Thr	Ser	Glu	Val	Tyr	Glu	Ile	Met	Val	Lys	Cys	Trp	Asn	Ser	
281					920					925						930	
283	gag	ccg	gag	aag	aga	ccc	tcc	ttt	tac	cac	ctg	agt	gag	att	gtg	gag	
284	Glu	Pro	Glu	Lys	Arg	Pro	Ser	Phe	Tyr	His	Leu	Ser	Glu	Ile	Val	Glu	
285					940					945						950	
287	aat	ctg	ctg	cct	gga	caa	tat	aaa	aag	agt	tat	gaa	aaa	att	cac	ctg	
288	Asn	Leu	Leu	Pro	Gly	Gln	Tyr	Lys	Lys	Ser	Tyr	Glu	Lys	Ile	His	Leu	
289					955					960						965	
291	gac	ttc	ctg	aag	agt	gac	cat	cct	gct	gtg	gca	cgc	atg	cgt	gtg	gac	
292	Asp	Phe	Leu	Lys	Ser	Asp	His	Pro	Ala	Val	Ala	Arg	Met	Arg	Val	Asp	
293					970					975						980	
295	tca	gac	aat	gca	tac	att	ggt	gtc	acc	tac	aaa	aac	gag	gaa	gac	aag	
296	Ser	Asp	Asn	Ala	Tyr	Ile	Gly	Val	Thr	Tyr	Lys	Asn	Glu	Glu	Asp	Lys	
297					985					990						995	
299	ctg	aag	gac	tgg	gag	ggt	ggt	ctg	gat	gag	cag	aga	ctg	agc	gct		
300	Leu	Lys	Asp	Trp	Glu	Gly	Gly	Leu	Asp	Glu	Gln	Arg	Leu	Ser	Ala		
301					1000					1005						1010	
303	gac	agt	ggc	tac	atc	att	cct	ctg	cct	gac	att	gac	cct	gtc	cct		3481
304	Asp	Ser	Gly	Tyr	Ile	Ile	Pro	Leu	Pro	Asp	Ile	Asp	Pro	Val	Pro		
305					1015					1020						1025	
307	gag	gag	gac	ctg	ggc	aag	agg	aac	aga	cac	agc	tcg	cag	acc		3526	
308	Glu	Glu	Glu	Asp	Leu	Gly	Lys	Arg	Asn	Arg	His	Ser	Ser	Gln	Thr		
309					1030					1035						1040	
311	tct	gaa	gag	agt	gcc	att	gag	acg	ggt	tcc	agc	agt	tcc	acc	tcc		3571
312	Ser	Glu	Glu	Ser	Ala	Ile	Glu	Thr	Gly	Ser	Ser	Ser	Ser	Ser	Thr	Phe	
313					1045					1050						1055	
315	atc	aag	aga	gag	gac	gag	acc	att	gaa	gac	atc	gac	atg	atg	gac		3616
316	Ile	Lys	Arg	Glu	Asp	Glu	Thr	Ile	Glu	Asp	Ile	Asp	Met	Met	Asp		
317					1060					1065						1070	
319	gac	atc	ggc	ata	gac	tct	tca	gac	ctg	gtg	gaa	gac	agc	tcc	ctg		3661
320	Asp	Ile	Gly	Ile	Asp	Ser	Ser	Asp	Leu	Val	Glu	Asp	Ser	Phe	Leu		
321					1075					1080						1085	
323	taa	ctggccgatt	cgaggggtc	cttcacttc	tggggccacc	tctggatccc											3714
325	gttcagaaaa	ccactttatt	gcaatgcgga	ggttgagagg	aggacttggt	tgtatgtttaa											3774

(from sequence 19)

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6

tgtatttgg tttttata g ca aca tca gag ctg gat cta gaa atg gaa 6183  
Ala Thr Ser Glu Leu Asp Leu Glu Met Glu  
insert → 210 215

gct ctt aaa acc gtg tat aag tca ggg gaa acg att gtg gtc acc tgt 6231  
Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys  
220 225 230 235

The above is a sample of several  
amino acid numbers inserted in  
sequence 19.

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/517,905

DATE: 12/22/2004  
TIME: 16:05:54

Input Set : A:\335026.txt  
Output Set: N:\CRF4\12222004\J517905.raw

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/517,905

DATE: 12/22/2004  
TIME: 16:05:54

Input Set : A:\335026.txt  
Output Set: N:\CRF4\12222004\J517905.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:4793 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
L:4794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:4901 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
L:4972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:10557  
M:341 Repeated in SeqNo=19  
L:10171 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
L:10246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:10328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:10740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:10886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:13371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:2047  
M:341 Repeated in SeqNo=26  
L:13881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:544  
M:341 Repeated in SeqNo=27